

SEQUENCE LISTING

<110> Estell, David A.

<120> Proteases From Gram-Positive Organisms

<130> GC381-US

<140> US 09/462,846

<141> 2000-01-13

<150> PCT/US98/19529

<151> 1998-07-14

<150> EP 97305227.7

<151> 1997-07-15

<160> 7

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 945

<212> DNA

<213> Bacillus subtilis

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gccgcgcataaaaatggtca aagcgttgtt caaaacggaa tgtataaggg	gttcacgctc	180
agcgaattat gggAACATCA cagacattta ttccggacagc ttgaagggg	ccgtttccct	240
ctgcttacaa aaatattttaga tgctgaccag gacttatctg ttccggatgc	tccgaatgtat	300
aatatgcacatacatga aaacggtgag ctggaaaaaa cagaatgtcg	gtacattatt	360
gattgccaaa aagatgccga gattattat ggccacaatg caacaacaaa	ggaagaacta	420
actaccatga tagagcgtgg agaatgggat gagcttgc gccgtgtaaa	ggtaaagccg	480
ggggattttt tctatgtgcc aagcggtaact gttcatgcga ttggaaaagg	aattcttgct	540
ttggagacgc agcagaactc agacacaacc tacagattat atgattatga	ccgaaaagat	600
gcagaaggca agctgcgcga gttcatctg aaaaagagca ttgaagtgt	agaggccccg	660
tctattccag aacggcatac agttcaccat gaacaaattt aggatttgct	tacaacgaca	720
ttgattgaat gcgcttactt ttccgggggg aaatggact tatcaggatc	agcaagctt	780
aaggcagcaaa aaccattcct tcttatacgt gtgattgaag gggagggccg	tatgatctct	840
ggtgagttatg tctatcctt caaaaaagga gatcatatgt tgctgcctt	cggctttggaa	900
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<210> 2

<211> 315

<212> PRT

<213> Bacillus subtilis

<400> 2

Met Thr Thr Glu Pro Leu Phe Phe Lys Pro Val Phe Lys Glu Arg Ile			
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Trp Gly Gly Thr Ala Leu Ala Asp Phe Gly Tyr Thr Ile Pro Ser Gln			
20	25	30	

Arg Thr Gly Glu Cys Trp Ala Phe Ala Ala His Gln Asn Gly Gln Ser			
35	40	45	

Val Val Gln Asn Gly Met Tyr Lys Gly Phe Thr Leu Ser Glu Leu Trp  
   50                       55                       60  
 Glu His His Arg His Leu Phe Gly Gln Leu Glu Gly Asp Arg Phe Pro  
   65                       70                       75                       80  
 Leu Leu Thr Lys Ile Leu Asp Ala Asp Gln Asp Leu Ser Val Gln Val  
   85                       90                       95  
 His Pro Asn Asp Glu Tyr Ala Asn Ile His Glu Asn Gly Glu Leu Gly  
  100                      105                       110  
 Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Gln Lys Asp Ala Glu Ile  
  115                      120                       125  
 Ile Tyr Gly His Asn Ala Thr Thr Lys Glu Glu Leu Thr Thr Met Ile  
  130                      135                       140  
 Glu Arg Gly Glu Trp Asp Glu Leu Leu Arg Arg Val Lys Val Lys Pro  
  145                      150                       155                       160  
 Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Val His Ala Ile Gly Lys  
  165                      170                       175  
 Gly Ile Leu Ala Leu Glu Thr Gln Gln Asn Ser Asp Thr Thr Tyr Arg  
  180                      185                       190  
 Leu Tyr Asp Tyr Asp Arg Lys Asp Ala Glu Gly Lys Leu Arg Glu Leu  
  195                      200                       205  
 His Leu Lys Lys Ser Ile Glu Val Ile Glu Val Pro Ser Ile Pro Glu  
  210                      215                       220  
 Arg His Thr Val His His Glu Gln Ile Glu Asp Leu Leu Thr Thr Thr  
  225                      230                       235                       240  
 Leu Ile Glu Cys Ala Tyr Phe Ser Val Gly Lys Trp Asn Leu Ser Gly  
  245                      250                       255  
 Ser Ala Ser Leu Lys Gln Gln Lys Pro Phe Leu Leu Ile Ser Val Ile  
  260                      265                       270  
 Glu Gly Glu Gly Arg Met Ile Ser Gly Glu Tyr Val Tyr Pro Phe Lys  
  275                      280                       285  
 Lys Gly Asp His Met Leu Leu Pro Tyr Gly Leu Gly Glu Phe Lys Leu  
  290                      295                       300  
 Glu Gly Tyr Ala Glu Cys Ile Val Ser His Leu  
  305                      310                       315

<210> 3  
 <211> 220  
 <212> PRT  
 <213> Bacillus subtilis

<400> 3

Val Leu Asn Asp Gly Asp Val Asn Ile Pro Glu Tyr Val Asp Trp Arg  
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  20                      25                       30  
 Cys Trp Ala Phe Ser Ala Val Val Thr Ile Glu Gly Ile Ile Lys Ile  
  35                      40                       45  
 Arg Thr Gly Asn Leu Asn Glu Tyr Ser Glu Gln Glu Leu Leu Asp Cys  
  50                      55                       60  
 Asp Arg Arg Ser Tyr Gly Cys Asn Gly Gly Tyr Pro Trp Ser Ala Leu  
  65                      70                       75                       80  
 Gln Leu Val Ala Gln Tyr Gly Ile His Tyr Arg Asn Thr Tyr Pro Tyr  
  85                      90                       95  
 Glu Gly Val Gln Arg Tyr Cys Arg Ser Arg Glu Lys Gly Pro Tyr Ala  
  100                     105                       110  
 Ala Lys Thr Asp Gly Val Arg Gln Val Gln Pro Tyr Asn Glu Gly Ala  
  115                     120                       125

Leu Leu Tyr Ser Ile Ala Asn Gln Pro Val Ser Val Val Leu Glu Ala  
   130                         135                         140  
 Ala Gly Lys Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro  
   145                         150                         155                         160  
 Cys Gly Asn Lys Val Asp His Ala Val Ala Ala Val Gly Tyr Gly Pro  
           165                         170                         175  
 Asn Tyr Ile Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn  
           180                         185                         190  
 Gly Tyr Ile Arg Ile Lys Arg Gly Thr Gly Asn Ser Tyr Gly Val Cys  
           195                         200                         205  
 Gly Leu Tyr Thr Ser Ser Phe Tyr Pro Val Lys Asn  
           210                         215                         220

<210> 4  
 <211> 948  
 <212> DNA  
 <213> *Bacillus subtilis*

<400> 4

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atttccgctc atccaaaagg accgagcact gttgcaaatg gccccgtataa aggaaaagaca	180
ttgatcgagc tttgggaaga gcaccgtgaa gtattcggcg gcgttagaggg ggatcggtt	240
ccgcttctga caaagctgct ggatgtgaag gaagatacgt caattaaagt tcaccctgat	300
gattactatg ccggagaaaa cgaagaggga gaactcggca agacggaatg ctgg tacatt	360
atcgactgta aggaaaacgc agaaaatcatt tacggcata cggcccgctc aaaaaccgaa	420
cttgcacaa tgatcaacag cggtgactgg gagggcctgc tgcgaagaat caaaattaaa	480
ccgggtgatt tctattatgt gccgagcggg acgctgcacg cattgtgcaa gggggccctt	540
gttttagaga ctcagcaaaa ttcatagatgcc acataccggg tgtacgatta tgaccgtctt	600
gatagcaacg gaagtccgag agagcttcat tttgccaag cggtaatgc cggcacgggtt	660
ccccatgtgg acgggtatat agatgaatcg acagaatcaa gaaaaggaat aaccattaaa	720
acatttgtcc aaggggaata ttttcggtt tataaatggg acatcaatgg cgaagctgaa	780
atggctcagg atgaatcctt tctgatttgc agcgtgatag aaggaagcgg tttgctcaag	840
tatgaggaca aaacatgtcc gtcaaaaaaaaa ggtgatcact ttatttgcc ggctcaaatg	900
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<210> 5  
 <211> 316  
 <212> PRT  
 <213> *Bacillus subtilis*

<400> 5

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Trp Gly Gly Thr Ala Leu Arg Asp Arg Phe Gly Tyr Ser Ile Pro Ser	
20                         25                         30	
Glu Ser Thr Gly Glu Cys Trp Ala Ile Ser Ala His Pro Lys Gly Pro	
35                         40                         45	
Ser Thr Val Ala Asn Gly Pro Tyr Lys Gly Lys Thr Leu Ile Glu Leu	
50                         55                         60	
Trp Glu Glu His Arg Glu Val Phe Gly Gly Val Glu Gly Asp Arg Phe	
65                         70                         75                         80	
Pro Leu Leu Thr Lys Leu Leu Asp Val Lys Glu Asp Thr Ser Ile Lys	
85                         90                         95	
Val His Pro Asp Asp Tyr Tyr Ala Gly Glu Asn Glu Glu Gly Glu Leu	
100                         105                         110	
Gly Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Glu Asn Ala Glu	

115	120	125
Ile Ile Tyr Gly His Thr Ala Arg Ser Lys Thr Glu Leu Val Thr Met		
130	135	140
Ile Asn Ser Gly Asp Trp Glu Gly Leu Leu Arg Arg Ile Lys Ile Lys		
145	150	155
Pro Gly Asp Phe Tyr Tyr Val Pro Ser Gly Thr Leu His Ala Leu Cys		
165	170	175
Lys Gly Ala Leu Val Leu Glu Thr Gln Gln Asn Ser Asp Ala Thr Tyr		
180	185	190
Arg Val Tyr Asp Tyr Asp Arg Leu Asp Ser Asn Gly Ser Pro Arg Glu		
195	200	205
Leu His Phe Ala Lys Ala Val Asn Ala Ala Thr Val Pro His Val Asp		
210	215	220
Gly Tyr Ile Asp Glu Ser Thr Glu Ser Arg Lys Gly Ile Thr Ile Lys		
225	230	235
Thr Phe Val Gln Gly Glu Tyr Phe Ser Val Tyr Lys Trp Asp Ile Asn		
245	250	255
Gly Glu Ala Glu Met Ala Gln Asp Glu Ser Phe Leu Ile Cys Ser Val		
260	265	270
Ile Glu Gly Ser Gly Leu Leu Lys Tyr Glu Asp Lys Thr Cys Pro Leu		
275	280	285
Lys Lys Gly Asp His Phe Ile Leu Pro Ala Gln Met Pro Asp Phe Thr		
290	295	300
Ile Lys Gly Thr Cys Thr Leu Ile Val Ser His Ile		
305	310	315

&lt;210&gt; 6

&lt;211&gt; 945

&lt;212&gt; DNA

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 6

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cttcgtgacg cttttggtca cgcaataccc tcacaaaaaa caggtgagtg ctggggcggtt	120
tctgcacatg cccatggctc gtcgtctgtt aaaaatggcc cgctggcaagg aaagacactt	180
gatcaagtat ggaaagatca tccagagata ttcgggttcc cgatggtaa ggtgtttccg	240
ctgctggtaa agctgtggc cgcataatgt gatctctccg tgcaagtcca tcctgtatgt	300
gattatgcaa aactgcacga aaatggcgac cttggtaaaa cggagtgctg gtatatcatt	360
gattgcaaag atgacgccga actaattttt ggacatcatg caagcacaaa ggaagagttc	420
aaacaacgaa tagaaagcgg tgattggAAC gggctgctga ggcgaatcaa aatcaagcca	480
ggagatttct tttatgtgcc aagcggtaaca ctccatgctt tatgttaaggg aacccttgtc	540
cttgaatcc agcaaaaactc tgataacaaca tatcgcttat acgattatga ccgctgtaat	600
gaccaggggcc aaaaaagaac tcttcataata gaaaaagcca tggaaagtcat aacgataccg	660
catatcgata aagtgcatac accggaagta aaagaagttt gtaacgctga gatcattgtt	720
tatgtgcaat cagattattt ctcagtgtac aaatgaaaga tttagcggccg agctgctttt	780
ccttcataatc aaacctattt gctggggagt gttctgagcg gatcaggacg aatcataaat	840
aatggatttc agtataaatg caatgcaggg tcacacttta ttctgcctgc gcattttgga	900
gaatttacaa tagaaggaac atgtgaattt atgatatctc atcct	945

&lt;210&gt; 7

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 7

Met Thr His Pro Leu Phe Leu Glu Pro Val Phe Lys Glu Arg Leu Trp			
1	5	10	15

Gly Gly Thr Lys Leu Arg Asp Ala Phe Gly Tyr Ala Ile Pro Ser Gln  
20 25 30  
Lys Thr Gly Glu Cys Trp Ala Val Ser Ala His Ala His Gly Ser Ser  
35 40 45  
Ser Val Lys Asn Gly Pro Leu Ala Gly Lys Thr Leu Asp Gln Val Trp  
50 55 60  
Lys Asp His Pro Glu Ile Phe Gly Phe Pro Asp Gly Lys Val Phe Pro  
65 70 75 80  
Leu Leu Val Lys Leu Leu Asp Ala Asn Met Asp Leu Ser Val Gln Val  
85 90 95  
His Pro Asp Asp Asp Tyr Ala Lys Leu His Glu Asn Gly Asp Leu Gly  
100 105 110  
Lys Thr Glu Cys Trp Tyr Ile Ile Asp Cys Lys Asp Asp Ala Glu Leu  
115 120 125  
Ile Leu Gly His His Ala Ser Thr Lys Glu Glu Phe Lys Gln Arg Ile  
130 135 140  
Glu Ser Gly Asp Trp Asn Gly Leu Leu Arg Arg Ile Lys Ile Lys Pro  
145 150 155 160  
Gly Asp Phe Phe Tyr Val Pro Ser Gly Thr Leu His Ala Leu Cys Lys  
165 170 175  
Gly Thr Leu Val Leu Glu Ile Gln Gln Asn Ser Asp Thr Thr Tyr Arg  
180 185 190  
Val Tyr Asp Tyr Asp Arg Cys Asn Asp Gln Gly Gln Lys Arg Thr Leu  
195 200 205  
His Ile Glu Lys Ala Met Glu Val Ile Thr Ile Pro His Ile Asp Lys  
210 215 220  
Val His Thr Pro Glu Val Lys Glu Val Gly Asn Ala Glu Ile Ile Val  
225 230 235 240  
Tyr Val Gln Ser Asp Tyr Phe Ser Val Tyr Lys Trp Lys Ile Ser Gly  
245 250 255  
Arg Ala Ala Phe Pro Ser Tyr Gln Thr Tyr Leu Leu Gly Ser Val Leu  
260 265 270  
Ser Gly Ser Gly Arg Ile Ile Asn Asn Gly Ile Gln Tyr Glu Cys Asn  
275 280 285  
Ala Gly Ser His Phe Ile Leu Pro Ala His Phe Gly Glu Phe Thr Ile  
290 295 300  
Glu Gly Thr Cys Glu Phe Met Ile Ser His Pro  
305 310 315